

Martin S Taylor

List of Publications by Year in descending order

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75
papers

16,427
citations

87723

38
h-index

79541

73
g-index

89
all docs

89
docs citations

89
times ranked

25390
citing authors

#	ARTICLE	IF	CITATIONS
1	The Transcriptional Landscape of the Mammalian Genome. <i>Science</i> , 2005, 309, 1559-1563.	6.0	3,227
2	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. <i>Nature</i> , 2004, 428, 493-521.	13.7	1,943
3	A promoter-level mammalian expression atlas. <i>Nature</i> , 2014, 507, 462-470.	13.7	1,838
4	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs. <i>Nature</i> , 2002, 420, 563-573.	13.7	1,548
5	Genome-wide analysis of mammalian promoter architecture and evolution. <i>Nature Genetics</i> , 2006, 38, 626-635.	9.4	1,201
6	Disruption of two novel genes by a translocation co-segregating with schizophrenia. <i>Human Molecular Genetics</i> , 2000, 9, 1415-1423.	1.4	1,135
7	Genome-wide genetic association of complex traits in heterogeneous stock mice. <i>Nature Genetics</i> , 2006, 38, 879-887.	9.4	508
8	The transcriptional network that controls growth arrest and differentiation in a human myeloid leukemia cell line. <i>Nature Genetics</i> , 2009, 41, 553-562.	9.4	408
9	Enzymatic Removal of Ribonucleotides from DNA Is Essential for Mammalian Genome Integrity and Development. <i>Cell</i> , 2012, 149, 1008-1022.	13.5	397
10	Conservation and divergence in Toll-like receptor 4-regulated gene expression in primary human versus mouse macrophages. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E944-53.	3.3	332
11	A High-Resolution Single Nucleotide Polymorphism Genetic Map of the Mouse Genome. <i>PLoS Biology</i> , 2006, 4, e395.	2.6	243
12	Lagging-strand replication shapes the mutational landscape of the genome. <i>Nature</i> , 2015, 518, 502-506.	13.7	213
13	CEP152 is a genome maintenance protein disrupted in Seckel syndrome. <i>Nature Genetics</i> , 2011, 43, 23-26.	9.4	201
14	Variant detection sensitivity and biases in whole genome and exome sequencing. <i>BMC Bioinformatics</i> , 2014, 15, 247.	1.2	197
15	Identification of a new gene mutated in Fraser syndrome and mouse myelencephalic blebs. <i>Nature Genetics</i> , 2005, 37, 520-525.	9.4	148
16	Genetic heterogeneity in Cornelia de Lange syndrome (CdLS) and CdLS-like phenotypes with observed and predicted levels of mosaicism. <i>Journal of Medical Genetics</i> , 2014, 51, 659-668.	1.5	141
17	The structure and evolution of the melanocortin and MCH receptors in fish and mammals. <i>Genomics</i> , 2003, 81, 184-191.	1.3	139
18	Identification of Common Genetic Variation That Modulates Alternative Splicing. <i>PLoS Genetics</i> , 2007, 3, e99.	1.5	139

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19	Genetic Analysis of Pathways Regulated by the von Hippel-Lindau Tumor Suppressor in <i>Caenorhabditis elegans</i> . <i>PLoS Biology</i> , 2004, 2, e289.	2.6	137
20	Characterization and comparative analysis of the EGLN gene family. <i>Gene</i> , 2001, 275, 125-132.	1.0	130
21	Occurrence and Consequences of Coding Sequence Insertions and Deletions in Mammalian Genomes. <i>Genome Research</i> , 2004, 14, 555-566.	2.4	114
22	Development and evaluation of a real-time PCR assay for detection of <i>Pneumocystis jirovecii</i> DNA in bronchoalveolar lavage fluid of HIV-infected patients. <i>Thorax</i> , 2007, 63, 154-159.	2.7	110
23	Functional annotation of human long noncoding RNAs via molecular phenotyping. <i>Genome Research</i> , 2020, 30, 1060-1072.	2.4	109
24	The extracellular matrix gene <i>Frem1</i> is essential for the normal adhesion of the embryonic epidermis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 13560-13565.	3.3	108
25	Evolution of the human-specific microRNA miR-941. <i>Nature Communications</i> , 2012, 3, 1145.	5.8	103
26	Heterotachy in Mammalian Promoter Evolution. <i>PLoS Genetics</i> , 2006, 2, e30.	1.5	102
27	Heterozygous Loss-of-Function Mutations in <i>YAP1</i> Cause Both Isolated and Syndromic Optic Fissure Closure Defects. <i>American Journal of Human Genetics</i> , 2014, 94, 295-302.	2.6	93
28	Evolutionary constraints on the Disrupted in Schizophrenia locus. <i>Genomics</i> , 2003, 81, 67-77.	1.3	83
29	Monoallelic and Biallelic Mutations in <i>MAB21L2</i> Cause a Spectrum of Major Eye Malformations. <i>American Journal of Human Genetics</i> , 2014, 94, 915-923.	2.6	79
30	Mutational Biases Drive Elevated Rates of Substitution at Regulatory Sites across Cancer Types. <i>PLoS Genetics</i> , 2016, 12, e1006207.	1.5	75
31	Quantifying single nucleotide variant detection sensitivity in exome sequencing. <i>BMC Bioinformatics</i> , 2013, 14, 195.	1.2	74
32	High resolution mapping of expression QTLs in heterogeneous stock mice in multiple tissues. <i>Genome Research</i> , 2009, 19, 1133-1140.	2.4	69
33	Pervasive haplotypic variation in the spliceo-transcriptome of the human major histocompatibility complex. <i>Genome Research</i> , 2011, 21, 1042-1054.	2.4	63
34	Codon Usage and Splicing Jointly Influence mRNA Localization. <i>Cell Systems</i> , 2020, 10, 351-362.e8.	2.9	61
35	Interaction of the Anaphase-promoting Complex/Cyclosome and Proteasome Protein Complexes with Multiubiquitin Chain-binding Proteins. <i>Journal of Biological Chemistry</i> , 2003, 278, 16791-16796.	1.6	60
36	Application of next generation qPCR and sequencing platforms to mRNA biomarker analysis. <i>Methods</i> , 2013, 59, 89-100.	1.9	55

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37	The frequent evolutionary birth and death of functional promoters in mouse and human. <i>Genome Research</i> , 2015, 25, 1546-1557.	2.4	55
38	Bidirectional transcription initiation marks accessible chromatin and is not specific to enhancers. <i>Genome Biology</i> , 2017, 18, 242.	3.8	52
39	Aberrant ribonucleotide incorporation and multiple deletions in mitochondrial DNA of the murine MPV17 disease model. <i>Nucleic Acids Research</i> , 2017, 45, 12808-12815.	6.5	43
40	Genome-wide mapping of embedded ribonucleotides and other noncanonical nucleotides using emRiboSeq and EndoSeq. <i>Nature Protocols</i> , 2015, 10, 1433-1444.	5.5	42
41	FRA2A Is a CCG Repeat Expansion Associated with Silencing of AFF3. <i>PLoS Genetics</i> , 2014, 10, e1004242.	1.5	41
42	Quantification of epigenetic biomarkers: an evaluation of established and emerging methods for DNA methylation analysis. <i>BMC Genomics</i> , 2014, 15, 1174.	1.2	40
43	Singleton SNPs in the human genome and implications for genome-wide association studies. <i>European Journal of Human Genetics</i> , 2008, 16, 506-515.	1.4	39
44	Signatures of TOP1 transcription-associated mutagenesis in cancer and germline. <i>Nature</i> , 2022, 602, 623-631.	13.7	38
45	Identification of a localized nonsense-mediated decay pathway at the endoplasmic reticulum. <i>Genes and Development</i> , 2020, 34, 1075-1088.	2.7	37
46	Pervasive lesion segregation shapes cancer genome evolution. <i>Nature</i> , 2020, 583, 265-270.	13.7	36
47	Sequence Characterization of Teleost Fish Melanocortin Receptors. <i>Annals of the New York Academy of Sciences</i> , 2003, 994, 319-330.	1.8	30
48	Genomic anatomy of the <i>Tyrp1</i> (brown) deletion complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 3704-3709.	3.3	30
49	Comparative transcriptomics of primary cells in vertebrates. <i>Genome Research</i> , 2020, 30, 951-961.	2.4	29
50	A CCG-Repeat Expansion Mutation in <i>ZNF713</i> Causes FRA7A: Association with Autistic Spectrum Disorder in two Families. <i>Human Mutation</i> , 2014, 35, n/a-n/a.	1.1	28
51	The severe G480C cystic fibrosis mutation, when replicated in the mouse, demonstrates mistrafficking, normal survival and organ-specific bioelectrics. <i>Human Molecular Genetics</i> , 2002, 11, 243-251.	1.4	27
52	Homozygous loss-of-function variants in European cosmopolitan and isolate populations. <i>Human Molecular Genetics</i> , 2015, 24, 5464-5474.	1.4	27
53	Genomic Sequence Analysis of <i>Fugu rubripes</i> CFTR and Flanking Genes in a 60 kb Region Conserving Synteny with 800 kb of Human Chromosome 7. <i>Genome Research</i> , 2000, 10, 1194-1203.	2.4	26
54	Dynamic and Physical Clustering of Gene Expression during Epidermal Barrier Formation in Differentiating Keratinocytes. <i>PLoS ONE</i> , 2009, 4, e7651.	1.1	26

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55	Expression of the <i>fras1/frem</i> gene family during zebrafish development and fin morphogenesis. <i>Developmental Dynamics</i> , 2008, 237, 3295-3304.	0.8	20
56	Loss of <i>ALDH18A1</i> function is associated with a cellular lipid droplet phenotype suggesting a link between autosomal recessive cutis laxa type 3A and Warburg Micro syndrome. <i>Molecular Genetics & Genomic Medicine</i> , 2014, 2, 319-325.	0.6	19
57	Rapidly evolving human promoter regions. <i>Nature Genetics</i> , 2008, 40, 1262-1263.	9.4	18
58	Increased ultra-rare variant load in an isolated Scottish population impacts exonic and regulatory regions. <i>PLoS Genetics</i> , 2019, 15, e1008480.	1.5	17
59	The (non)malignancy of cancerous amino acidic substitutions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 518-529.	1.5	15
60	SuRFing the genomics wave: an R package for prioritising SNPs by functionality. <i>Genome Medicine</i> , 2014, 6, 79.	3.6	15
61	Isolation and characterization of the mouse translin-associated protein X (Trax) gene. <i>Mammalian Genome</i> , 2000, 11, 395-398.	1.0	12
62	Manipulation of Dipeptidylpeptidase 10 in mouse and human <i>in vivo</i> and <i>in vitro</i> models indicates a protective role in asthma. <i>DMM Disease Models and Mechanisms</i> , 2018, 11, .	1.2	11
63	<i>In Vivo</i> Modeling of Patient Genetic Heterogeneity Identifies New Ways to Target Cholangiocarcinoma. <i>Cancer Research</i> , 2022, 82, 1548-1559.	0.4	8
64	The Structure of Change. <i>Science</i> , 2009, 323, 347-348.	6.0	7
65	Functional analysis of a novel ENU-induced PHD finger 11 (Phf11) mouse mutant. <i>Mammalian Genome</i> , 2014, 25, 573-582.	1.0	7
66	Exome Sequencing to Detect Rare Variants Associated With General Cognitive Ability: A Pilot Study. <i>Twin Research and Human Genetics</i> , 2015, 18, 117-125.	0.3	7
67	Problems of Developing Molecular Diagnostic Tests for Opportunistic Pathogens: The Example of <i>Pneumocystis jirovecii</i> . <i>Journal of Eukaryotic Microbiology</i> , 2006, 53, S85-S86.	0.8	4
68	Management, presentation and interpretation of genome scans using GSCANDB. <i>Bioinformatics</i> , 2007, 23, 1545-1549.	1.8	4
69	Mutational bias in spermatogonia impacts the anatomy of regulatory sites in the human genome. <i>Genome Research</i> , 2021, 31, 1994-2007.	2.4	4
70	The contribution of evolutionarily volatile promoters to molecular phenotypes and human trait variation. <i>Genome Biology</i> , 2022, 23, 89.	3.8	4
71	Sushi gets serious: the draft genome sequence of the pufferfish <i>Fugu rubripes</i> . <i>Genome Biology</i> , 2002, 3, reviews1025.1.	13.9	1
72	Evidence of a Large-Scale Functional Organization of Mammalian Chromosomes: Authors' Reply. <i>PLoS Biology</i> , 2007, 5, e128.	2.6	1

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73	Comparative Genomics. , 0, , 105-144.		0
74	Comparative Genomics and Mammalian Promoter Evolution. , 2009, , 209-226.		0
75	Evolutionary dependencies show paths to cancer development. Nature Genetics, 2020, 52, 1135-1136.	9.4	0